
Supplementary information

Genetic architecture in Greenland is shaped by demography, structure and selection

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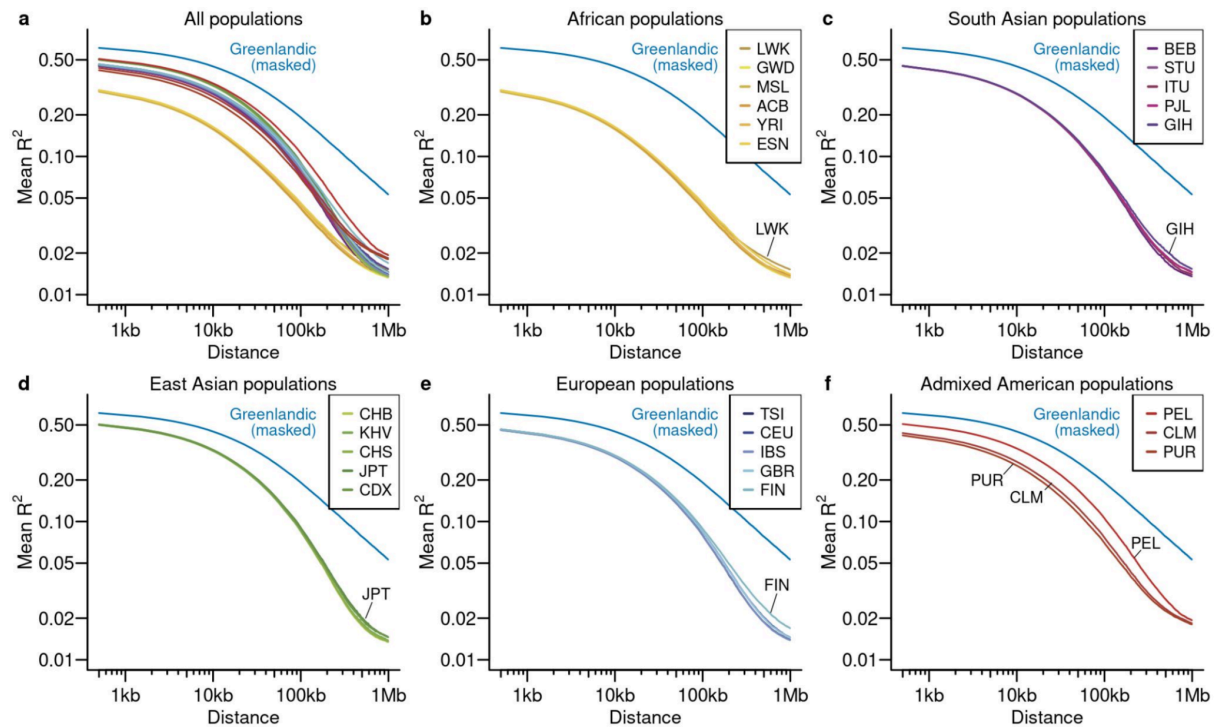
Supplementary text

Non-peer reviewed summary in Greenlandic - Kalaallisut naalisarnera

Kalaallit / inuit nunallu inoqqaavi allat, pinngoqqaatinik ilisimatusarnermi peqataatinneqarpiangillat. Taamaammat kalaallit 448-it pinngoqqaataat ataatsimoortut- sananeqaataasa tulleriinneri qulaajarlugillu misissoqqissaarpagut. Oqaluttuarisaanikkut innuttaasut ikittunnguunerisa, Europamut sanilliullugit nunatsinni pinngoqqaatini allannguutit ikinnerunerannik nassataqarnera, takutipparput. Europamili allannguutit amerlasuut nalinginnaasumik ikittunit pigineqartarnerannut sanilliullugit, nunatsinni allannguutit ilarpassui amerlasuunit pigineqarput. Allannguutit ikinnerugaluit, nunatsinni allannguutit suussusersisagut timip sulinerata inooriaatsimut attuumassuteqartup akornuteqarnera Europamiittunit pingaaruteqarneruvoq. Pinngoqqaatini allannguutit annertuumik pingaarutillit, inuit siuliisa Amerikami nunap inoqqaavinit avissaarnerisa kingorna pinngorsimanissaat ilimagaarput. Taamaammat allannguutit issittuni innuttaasuni atuupput. Pinngoqqaatini allannguutit taakku ilaasa oqaluttuarisaanermi innuttaasut ikittunnguusimanerat pissutigalugu amerlasuunit pigineqarnerat, allannguutillu ilaat allat pissusissamisoortumik ineriartornermit sunnerneqarsimanerattaaq takutipparput. Nappaatinik suussusersiniaanermi / aarlerinassutsimik naliliinermi sakkussat “Polygene scorer” Europamiunit pissarsiarineqartut, Europamiunut sanilliullugit kalaallini timip sulinerata akornuteqarneranik inooriaatsimut attuumassuteqartumik siulittuinissamut affaannarmik eqqortuunerat takutipparputtaa. Issittumili pinngoqqaatini allannguutit ilanngunnerisigut eqqussusaa Europamiutulli pitsanngorsinnaavoq. Pisortat pinngoqqaatit pillugit paasissutissiiviini amigaateqarnerup, pinngoqqaatinik misissuiniarneq Europamut sanilliullugu nunatsinni ajornakusoornerulersikkaa takutipparputtaa. Nunatsinni paasissutissanik ilanngussineq, allannguutit tamatumunnga attuumassuteqanngitsut arfinileriaammik ikilisitsinerup, misissuineramik annertuumik pitsaanerulersitsinera takutipparputtaa. Naggataagut nunatsinni pinngoqqaatit aaqqissuussaanagerat, nunarput akimorlugu nappaatit kingornuttakkat, pinngoqqaatip attaatsip allannguuteqarneranik patsiseqartut atugaanerisa assigiinngissutaannut nassuiaataasoq, suussusersivarput. Siunissami nappaatit kinguaariinni kingusinnerusuni takkuttartut ilaasa, nunatta iluani nuttarnerulerneq pissutigalugu, aarlerinaatip annikillinissaa siulittuutigaarput. Ataatsimut isigalugu ilisimatusarnerni paasissutissiivinnilu kalaallinik peqataatitsinerup pinngoqqaatinik tunngaveqartumik peqqissaanermi naligiinngitsumik pineqarnissamik pitsaaleeqataasinnaanera, misissuinitinni paasisatta takutippaat.

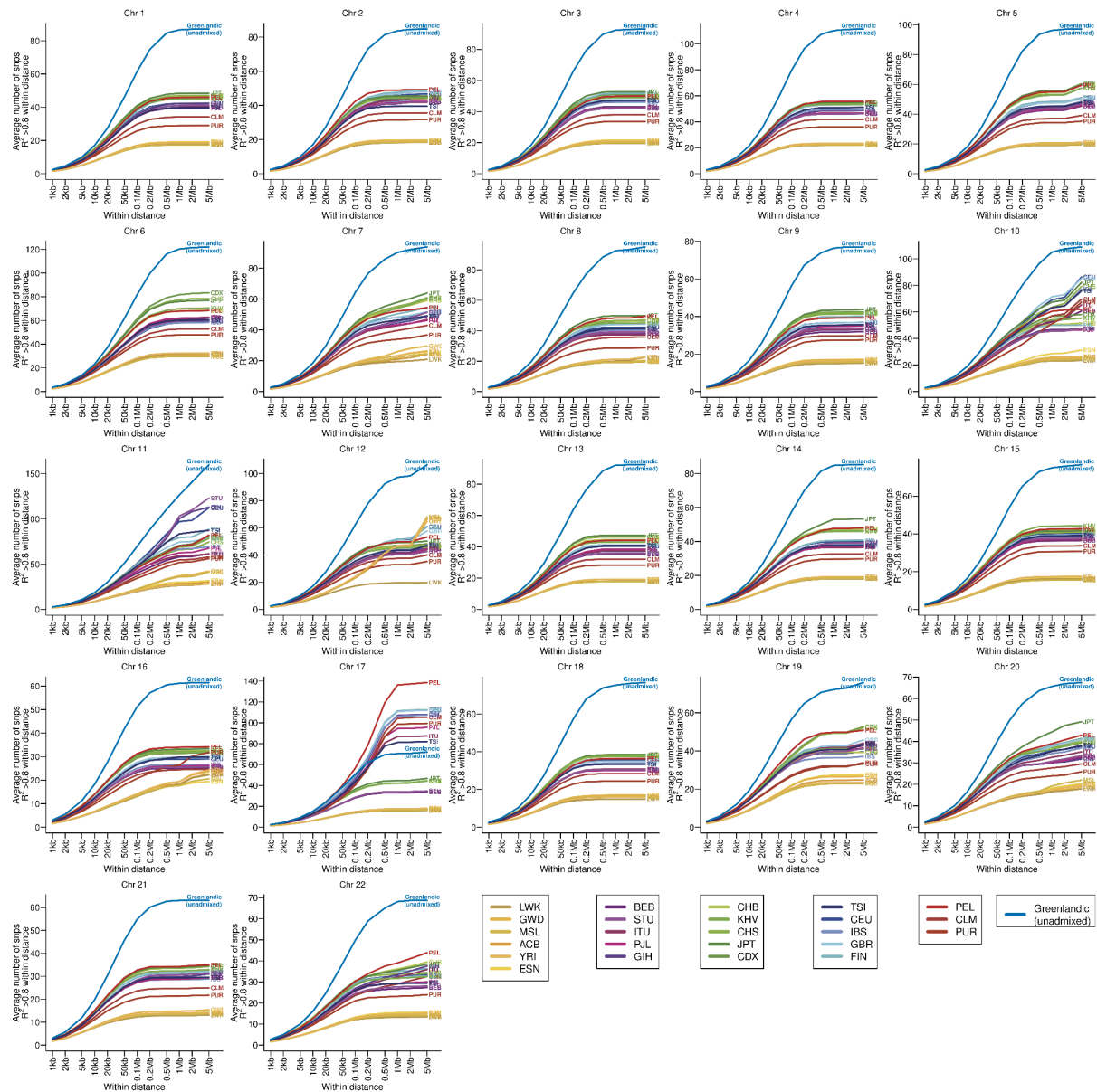
Supplementary Figures

Supplementary Figure 1



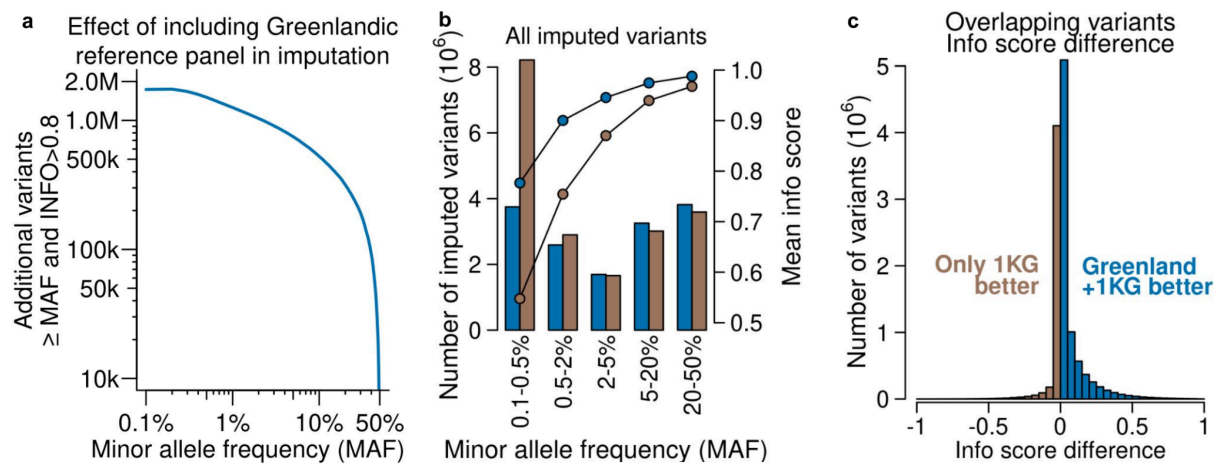
Supplementary figure 1. Linkage disequilibrium decay. Mean r^2 as a function of distance from focal SNP for all 1KG populations and Greenlandic Inuit. Randomly subsampled $n=85$ per population except ASW and MXL which had only $n=61$ and $n=64$ available, respectively.

Supplementary Figure 2



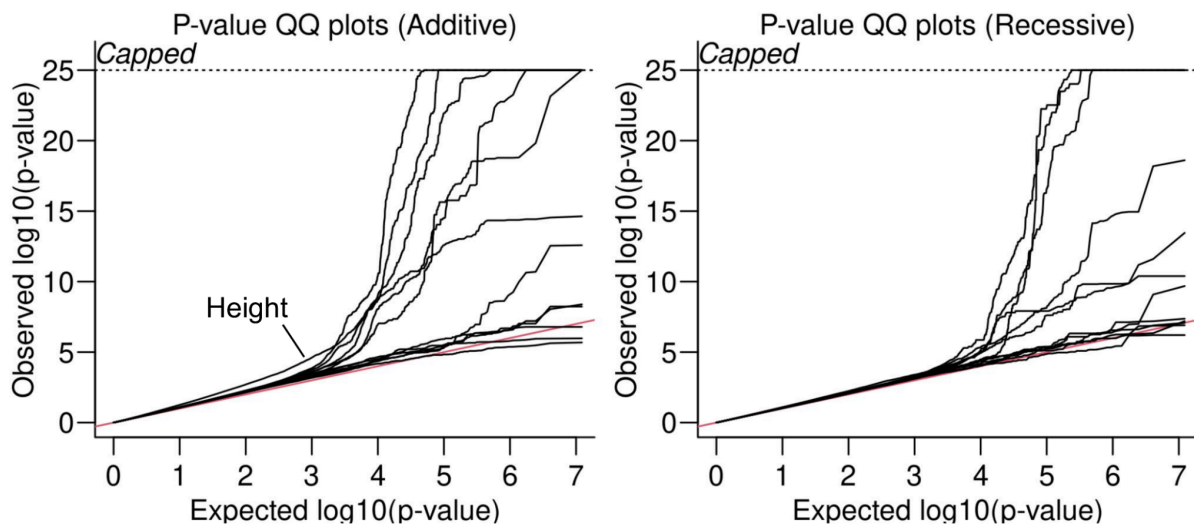
Supplementary figure 2. Mean number of tag-SNPs ($r^2 > 0.8$) for all 1KG populations and Greenlandic Inuit per chromosome. $N=85$ per population. Randomly subsampled $N=85$ per population except ASW and MXL which had only $n=61$ and $n=64$ available, respectively.

Supplementary Figure 3



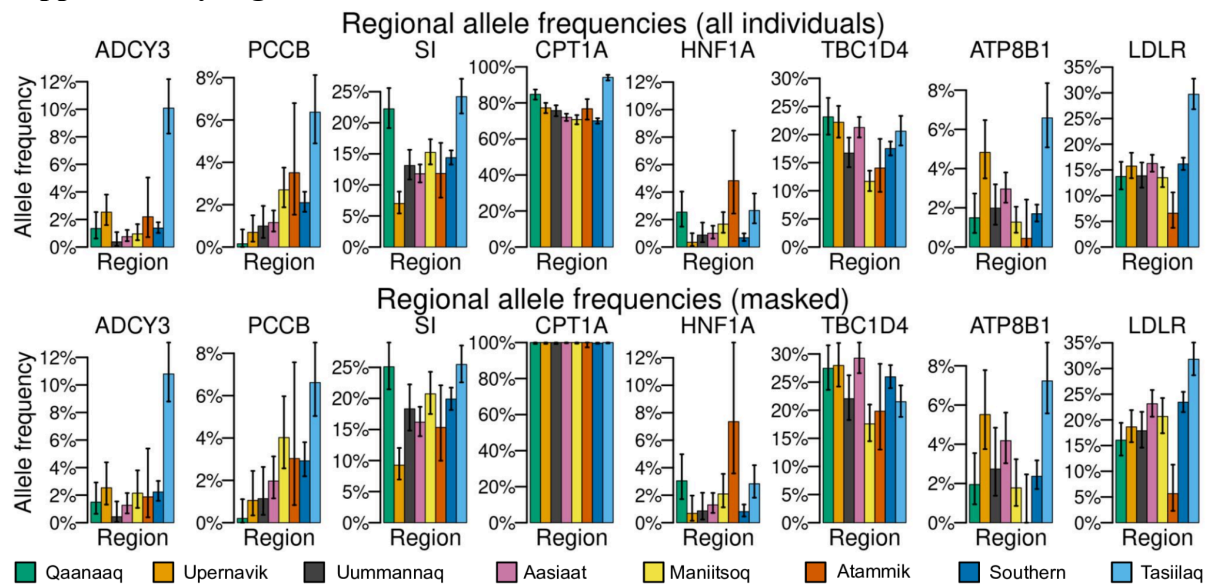
Supplementary figure 3. Imputation of 5,548 individuals with both Greenlandic WGS plus 1KG (blue, n=448+3202) or only the 1KG reference (brown, n=3202). Imputed MAF. **a**, The number of additional variants accurately called variants (INFO>0.8) when adding the Greenlandic reference panel to the imputation. **b**, Number of imputed variants as barplots in frequency bins and corresponding mean imputation score as lines. **c**, histogram of info score difference for overlapping variants.

Supplementary Figure 4



Supplementary figure 4. P-value QQ plots from GWAS on 13 metabolic traits. As can be seen there is no inflation for any of the traits except for height, which is known to be highly polygenic.

Supplementary Figure 5



Supplementary figure 5. Regional allele frequency estimates of the eight high impact Arctic-specific variants. Bottom row is allele frequency estimates from the masked Greenlandic data, excluding any European ancestry. Error bars show the 95% confidence interval.